

BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN OB-CADHERIN-1 POLYPEPTIDE SEQ ID NO: 16

Query: Cadherin-like plypeptide (SEQ ID NO: 4)
 Subjct: dbj|BAA04798.1| (D21254) OB-cadherin-1 [Homo sapiens] (SEQ ID NO: 16)
 Length = 796

Score = 1478 (525.3 bits), Expect = 2.1e-164, Sum P(2) = 2.1e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRRRSWVWNQFFVIEEYAGPEPVLIGKLHSDVDRGGRKYLTLTGEGAGTVFVID 462
 G L R++R WYWNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjet: 45 GQVLQSRKRGWVWNQFFVIEEYTGPDVPLVGLHSDIDSDGDNIKYILSGEGAGTIFVID 104

Query: 463 EATGNIHVTKSLDREEKAQYVLLAQAVDRASNRPLEPPSEFIITKGQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRLEPPSEFI+K QDINDNPP F Y
 Sbjet: 105 DKSGNIHATKTLDREERAQYTLMAQAVDRDTRNPLEPPSEFIVKVDINDNPEEFLHETY 164

Query: 643 HATPEMSNVGTSVIQVTAHDADDPYSGNSAKLVYTVTLVDGLPFFSVDPQTGVVVRTALPNM 822
 HA VPE SNVGTSLVQVTA DADDP+YGNLAKLVY++L+G P+FSV+ QTG++RTA+PNM
 Sbjet: 165 HANVPERSNVGTSVIQVTAHDADDPYSGNSAKLVYTVTLVDGLPFFSVDPQTGVVVRTALPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGLSGSTTVTVTLSDVNDNPPKFPQSLYQFSVVETAGPG 1002
 DRE +EE+ VVIQAKDMGGMGLSG+T VT+TL+DVNDNPPKFPQS+YQ SV E A PG
 Sbjet: 225 DREAKEYHVVIQAKDMGGMGLSGTITLTVTLSDVNDNPPKFPQSVYQISVSEAAVPG 284

Query: 1003 TLVGRILRAQDPDLGDNALMAYSILDEGESEAFSISTDLQGRDGLLTVRKPLDFESQRSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjet: 285 EEVGRVKAKDPDIDENGGLVTVYNIVDGDMESFEITTDYETQEGVIKPKKPVDFETKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRRGPFKDVASVRVAVQDAPEPAFTQAAAYHLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjet: 345 LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAAGTVVGR 404

Query: 1363 ISAADLSPASPIRYSILPHSDPERCFSTIQPEEGTIHTAAPLDREARAWHNLTVLATEL 1539
 + A D+ SPIRYSI H+D +R F+I PE+G I T PLDR AW N+TV A E+
 Sbjet: 405 VHAKDPDAANSPIRYSIDRHTDLDRFFTNPEDGFIKTKPLDREETAWLNITVFAAEI 463

FIG. 1

**BLASTX ALIGNMENT OF SEQ ID NO: 4, CADHERIN-LIKE POLYPEPTIDE WITH HUMAN
SEQUENCE ENCODED BY HUMAN OSF-4-1 CDNA POLYPEPTIDE SEQ ID NO: 17**

Query: Cadherin-like pypeptide (SEQ ID NO: 4)
 Subject: sp|R49731|R49731 Sequence encoded by human OSF-4-1 Cdna (SEQ ID NO: 17)
 Length = 796

Score = 1478 (525.3 bits), Expect = 1.2e-164, Sum P(2) = 1.2e-164
 Identities = 269/419 (64%), Positives = 341/419 (81%), Frame = +1

Query: 283 GPALLRRSRWVNQFFVIEEYAGPEPVLICKLHSDVDREGRTKYLLTGEAGTVEFVID 462
 G L R++R WVNQFFVIEEY GP+PVL+G+LHSD+D G+G KY+L+GEGAGT+FVID
 Sbjct: 45 GQVLRSKRGWVNQFFVIEEYTGPDPLVGRHLHSDIDSQDGNIKYILSGEGAGTIFVID 104

Query: 463 EATGNIHVTKSLDREEKAQYVLLAQAVDRASNRPLEPPSEFIKQDINDNPPIFPLGPY 642
 + +GNIH TK+LDREE+AQY L+AQAVDR +NRPLEPPSEFI+K QDINDNPP F Y
 Sbjct: 105 DKSGNIHATKTLDREERAQYTLMAQAVDRDTRNPLEPPSEFIVKVQDINDNPPFLHETY 164

Query: 643 HATVPEMSNVGTSVIQVTAHDADDPYSGNSAKLYVTVDGLPFFSFVDPPQTGVVRTAIPNM 822
 HA VPE SNVGTSVIQVTA DADDP+YGNLAKLY++L+G P+FSV+ QTG++RTA+PNM
 Sbjct: 165 HANVPERSNVGTSVIQVTAHDADDPYSGNSAKLYVTVDGLPFFSFVDPPQTGVVRTAIPNM 224

Query: 823 DRETQEEFLVVIQAKDMGGMGGLSGSTTVTTLSDVNDNPPKFPQSLYQFSVVETAGPG 1002
 DRE +EE+ VVIQAKDMGGMGGLSG+T VT+TL+DVNDNPPKFPQSLYQ SV E A PG
 Sbjct: 225 DREAEEYHVVIIQAKDMGGMGGLSGTTKVTITLTDVNDNPPKFPQSLYQSVSEAAVPG 284

Query: 1003 TLVGRRLRAQDPDLGDNALMAYSIILDEGESEAFSISTDLQGRDGLLTVRKPLDFESQRSYS 1182
 VGR++A+DPD+G+N L+ Y+I+DG+G E+F I+TD + ++G++ ++KP+DFE++R+YS
 Sbjct: 285 EEVGRVKAKDPDIGNGLVTVYNIVDGDMESFEITTDYETQEGVIKPKPVDFTKRAYS 344

Query: 1183 FRVEATNTLIDPAYLRGPFKDVASVRVAVQDAPEPFAFTQAAAYHLLTVPENKAPGTLVGQ 1362
 +VEA N IDP ++ GPFKD +V++AV+DA EPP F +Y V EN A GT+VG+
 Sbjct: 345 LKVEAANVHIDPKFISNGPFKDTVTVKIAVEDADEPPMFLAPSYIHEVQENAAAAGTVVGR 404

Query: 1363 ISAADLSPASPIRYSILPHSDPERCFSIQPEEGTIHTAAPLDREARAWHLTVIATEL 1539
 + A D+ SPIRYSI H+D +R F+I PE+G I T PLDRE AW N+TV A E+
 Sbjct: 405 VHAKDPDAANSPIRYSIDRHTDLDRFTINPEDGFIKTKPLDREATAWLNITVFAAEI 463

FIG. 2